

ENHANCING LIPID PRODUCTION OF *PHAEODACTYLUM TRICORNUTUM* THROUGH METABOLIC ENGINEERING

Michiel Matthijs^{1,2,3}, Michele Fabris^{1,2,3}, Gino J.E. Baart^{1,2,3}, Alain Goossens^{1,2} & Wim Vyverman³

¹Department of Plant Systems Biology, VIB

²Department of Plant Biotechnology and Bioinformatics

³Laboratory of Protistology and Aquatic Ecology, Department of Biology, Ghent University

Diatoms hold much promise for the production of lipids and other metabolites. We apply a functional genomics approach using the model diatom *Phaeodactylum tricornutum* in order to identify the key regulator genes that drive lipid synthesis. To this end we are using RNA-seq to sequence the transcriptome of *P. tricornutum* during stress conditions and comparing these transcriptome profiles with non-lipid producing conditions. In this way we map the metabolic reprogramming that cells undergo during the switch from growth towards carbon storage and in particular lipid production. Since we are chiefly interested in the regulators involved in this reprogramming and, to a lesser degree, in the enzymes actually effectuating this change, we are performing our analysis during the first 24 hours of these lipid producing conditions when lipid productivity is only starting. In the second phase of the project we will attempt to activate this program during conditions that favor exponential growth using genetic engineering. Preliminary transcriptome analysis using cDNA-AFLP shows that 2-5% of genes respond to investigated stress conditions. Furthermore, metabolic analysis shows that there are quantitative changes detectable in chrysolaminaran and lipid storage products. These changes appear to be coupled to cell cycle progression. We have also shown for the first time that *P. tricornutum* lipid productivity can indeed be enhanced by overexpression of endogenous genes.